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OM nucleic - nucleic search, using sw model

Run on: September 1, 2000, 01:01:08 ; Search time 261.02 Seconds
                                              (without alignments)
                                              4319.238 Million cell updates/sec

Title: US-09-171-553-2
Perfect score: 8196
Sequence: 1 tgtgggcccagcgcgcttg.........aaaaaaaaaaaaaaaaa 8196
Scoring table: IDENTITY_NUC
Scoring table: Gapop 10.0 , Gapext 1.0
Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

num DB seq length: 0
imum DB seq length: 1000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%Query Match	Length	DB	DB ID	Description
1	2240.2	27.3	8535	5	US-08-716-351A-1	Sequence 1, Appli
2	1739.4	21.2	8323	4	US-08-110-300A-8	Sequence 8, Appli
3	1739.4	21.2	8323	4	US-08-886-642-8	Sequence 8, Appli
4	1739.4	21.2	8323	6	PCT-US99-08041-8	Sequence 8, Appli
5	1730	21.1	8202	6	US-08-258-420-13	Sequence 13, Appl
6	1678.6	20.5	8332	5	US-08-850-961-1	Sequence 1, Appli
7	1588.4	19.4	10367	4	US-08-110-300A-9	Sequence 9, Appli
8	1588.4	19.4	10367	5	US-08-886-642-9	Sequence 9, Appli
9	1588.4	19.4	10367	6	PCT-US93-08041-9	Sequence 9, Appli
10	842.2	10.3	3674	1	US-08-105-48J-324	Sequence 324, App
11	842.2	10.3	3674	2	US-08-709-209-324	Sequence 324, App
12	842.2	10.3	3674	2	US-08-458-101-324	Sequence 324, Appli
13	815.4	9.9	6363	5	US-08-929-967-6	Sequence 6, Appli
14	359.4	4.4	10970	5	US-08-716-351A-5	Sequence 5, Appli
15	303.8	3.7	1965	2	US-08-258-420-9	Sequence 9, Appli
16	301.4	3.7	2499	2	US-08-105-48J-310	Sequence 310, App
17	301.4	3.7	2499	2	US-08-709-209-310	Sequence 310, App
18	301.4	3.7	2499	2	US-08-458-101-310	Sequence 310, Appl
19	300.6	3.7	2001	5	US-08-850-961-13	Sequence 13, Appl
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22	298.2	3.5	1911	2	US-08-258-420-8	Sequence 8, Appli
23	290.2	3.5	1914	1	US-08-258-420-7	Sequence 7, Appli
24	274.8	3.4	789	1	US-08-181-335B-3	Sequence 3, Appli
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31	226.2	2.8	1234	2	US-08-798-000-1	Sequence 1, Appli
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37	162.6	2.0	8387	3	US-08-532-814-1	Sequence 1, Appli
38	157.2	1.9	10306	5	US-08-716-351A-4	Sequence 4, Appli
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44	149.6	1.8	1158	5	US-08-691-563C-1	Sequence 1, Appli
45	144.4	1.8	9661	5	US-08-716-351A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-716-351A-1
Sequence 1, Application US/08716351A
Patent No. 6033905
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian,, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "GaLV SEATO Genome"
US-08-716-351A-1

Query Match   27.3%; Score 2240.2; DB 5; Length 8535;
Best Local Similarity   59.0%;
Matches 4358; Conservative   2; Mismatches 2820; Indels 207; Gaps 22;

Qy 320 agcagacgtgctaggagatcacaggctgcaccctggggaacgccccgggaggtgggga 379
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Db   816  GGACCAGGAGGACCGCCTTGGGTGGACCCTCG----------GTAACGGGTTCGGTTGTGACCCG  864
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Qy  1634  atttcttgagaggctcatgaagcctcaggcggttcaccccttttgatctcctcaga  1693
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Qy   4512  aacgcccaaagcccagaacccagacgacagtacaaccctagaagaagaactggcaagagatcaa                                     4571
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Qy   4572  aaagatagaccaagttctctgagacctcggaggggggacctgctatacctcatatgggaagga                                      4631
Db   4972  -------------------------------                                                                     4971
Qy   4632  aatcctgcccacaaagagaggggttagaatatgtccaaaaagatacacatggtctaacccactt                                     4691
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About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
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Patent No. 6033905
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "GalV SEATO Genome"
US-08-716-351A-1

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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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; TITLE OF INVENTION: Retroviral Vectors
; NUMBER OF SEQUENCES: 5
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/716,351A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03784
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian,, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 15280-128-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
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; LENGTH: 8535 base pairs
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; LOCATION: 1..8535
; OTHER INFORMATION: /standard_name= "GaLV SEATO Genome"
US-08-716-351A-1

alignment_scores:
Quality: 1660.50   Length: 542
Ratio: 3.944   Gaps: 10
Percent Similarity: 77.675   Percent Identity: 61.439

alignment_block:
US-09-171-553-4 x US-08-716-351A-1

Align seq 1/1   to: US-08-716-351A-1   from: 1   to: 8535

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    1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpPth 17
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 1001 ATGGGACAAGATAAGATAATTCTACCCCCTATTCTCCCTCACTCTAAATCACTGGAG 1050

   17 rGluValArgSerArgAlaHisAsnLeuServalGlnValLysLysGlyP 34
        ||||||::|||||||||||||||||||||||||:::||||||||||||
 1051 AGATGTGAGACAAGGGCTCACAATCTATCCGTGGAAATCAAAAAGGGAA 1100

   34 roTrpGlnThrPheCysAlaserGluTrpProThrPheAspValGlyTrp 50
        ||||||||||||||::||||||||||||||||||||||| ||||||
 1101 AATGGCAGACTTTCTGTTTCCTCCGAGTGGCCCACAATTCGCGTGGGGTGG 1150

   51 ProSerGluGlyThrPheAsnSerGlulleIleLeuLeuAlaVallySAlaIl 67
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